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MAR 18 2004
PATENT & TRADEMARK

FASTA searches a protein or DNA sequence data bank
version 3.3t05 March 30, 2000

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp/fastaGAAosaW1G: 963 aa
>LEX 263 SEQ ID NO:2
vs /tmp/fastaHAApsaW1G library
searching /tmp/fastaHAApsaW1G library

956 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2
join: 39, opt: 27, gap-pen: -12/ -2, width: 16
Scan time: 0.033

The best scores are: opt
gi|12276180|gb|AAG50282.1|AF326918_1 metalloprote (956) 6778

>>gi|12276180|gb|AAG50282.1|AF326918_1 metalloprotease-d (956 aa)
initn: 5376 init1: 5315 opt: 6778
Smith-Waterman score: 6778; 98.755% identity in 964 aa overlap (1-963:1-956)

	10	20	30	40	50	
LEX	MPGGAGAARLCLLAFALQPLRPRAAREPGWT-RGSEEGSPKLQHELIIPQWKTSESPVRE					

gi 122	MPGGAGAARLCLLAFALQPLRPRAAREPGWTSKGSEEGSPKLQHELIIPQWKTSESPVRE					
	10	20	30	40	50	60
	60	70	80	90	100	110
LEX	KHPLKAELRVMAEGRELILDLEKNEQLFAPSYTETHYTSSGNPQTTTRKLEDHCFYHGTV					

gi 122	KHPLKAELRVMAEGRELILDLEKNEQLFAPSYTETHYTSSGNPQTTTRKLEDHCFYHGTV					
	70	80	90	100	110	120
	120	130	140	150	160	170
LEX	RETELSSVTLSTCRGIRGLITVSSNLSYVIEPLPDSKGQHLIYRSEHLKPPPGNCGFEHS					

gi 122	RETELSSVTLSTCRGIRGLITVSSNLSYVIEPLPDSKGQHLIYRSEHLKPPPGNCGFEHS					
	130	140	150	160	170	180
	180	190	200	210	220	230
LEX	KPTTRDWALQFTQQTKKRPRRMKREDLNSMKYVELYLVADYLEFQKNRRDQDATKHKLIE					

gi 122	KPTTRDWALQFTQQTKKRPRRMKREDLNSMKYVELYLVADYLEFQKNRRDQDATKHKLIE					
	190	200	210	220	230	240
	240	250	260	270	280	290
LEX	IANYVDKFYRSLNIRIALVGLVWTHGNMCEVSENPYSTLWSFLSWRRKLLAQKYHDNAQ					

gi 122	IANYVDKFYRSLNIRIALVGLVWTHGNMCEVSENPYSTLWSFLSWRRKLLAQKYHDNAQ					
	250	260	270	280	290	300
	300	310	320	330	340	350
LEX	LITGMSFHGTTIGLAPLMAMCSVYQSGGVNMDHSENAIGVAATMAHEMGMHNFMTSDSAD					

gi 122	LITGMSFHGTTIGLAPLMAMCSVYQSGGVNMDHSENAIGVAATMAHEMGMHNFMTSDSAD					
	310	320	330	340	350	360
	360	370	380	390	400	410
LEX	CCSASAADGGCIMAATGHPFPKVFNGCNRRRELDRLQSGGMCLSNMPDTRMLYGGRRRC					

3/11/2004

::::
gi|122 LVPA

963 residues in 1 query sequences



956 residues in 1 library sequences

Scomplib [version 3.3t05 March 30, 2000]

start: Thu Mar 11 14:41:49 2004 done: Thu Mar 11 14:41:50 2004

Scan time: 0.033 Display time: 1.317

Function used was FASTA



Entrez PubMed Nucleotide Protein Genome Structure PMC Taxonomy Boo

Search for

Limits Preview/Index History Clipboard Details

Show:

☐ 1: AAG50282. metalloprotease-d...[gi:12276180] BLink, Domains, Links

LOCUS AAG50282 956 aa linear PRI 13-JUL-2001

DEFINITION metalloprotease-disintegrin meltrin beta [Homo sapiens].

ACCESSION AAG50282

VERSION AAG50282.1 GI:12276180

DBSOURCE locus AF326918 accession AF326918.1

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (residues 1 to 956)

AUTHORS Wang, Y.-G. and Gong, L.

TITLE Identification of FKSG34, a novel human gene encoding for
metalloprotease-disintegrin meltrin beta

JOURNAL Unpublished

REFERENCE 2 (residues 1 to 956)

AUTHORS Wang, Y.-G.

TITLE Direct Submission

JOURNAL Submitted (07-DEC-2000) Beijing Fengkesheng Function Gene
Technology Ltd., 4 Tou Tiao Lu Chang Street, Xuanwu District,
Beijing 100050, P.R. China

COMMENT Method: conceptual translation.

FEATURES

source

1..956

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="5"

Protein

1..956

/product="metalloprotease-disintegrin meltrin beta"

CDS

1..956

/gene="FKSG34"

/coded_by="AF326918.1:46..2916"

ORIGIN

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121 retelssytl  stcrgirgli  tvssnlsyvi  eplpdskgqh  liyrsehlkp  ppgncgfehs
181 kpttrdwalq  ftqqtkkrpr  rmkredlnsm  kyvelylvad  ylefqknrrd  qdatkhklie
241 ianyvdkfyr  slnirialvg  levwthgnmc  evsenpystl  wsflswrrkl  laqkyhdnaq
301 litgmsfhgt  tiglaplmam  csvyqsggvn  mdhsenaigv  aatmahemgh  nfgmthdsad
361 ccsasaadgg  cimaaatghp  fpkvfngcnr  reldrylqsg  ggmclsnmpd  trmlyggrrc
421 gngyledgee  cdgeeeeecn  npccnasnct  lrpgaecahg  scchqcklla  pgtlcreqar
481 qcdlpeftg  kspheptnfy  qmdgtpcceg  qaycyngmcl  tygeqcqqlw  gpgarpapdl
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601 grqiqcrgh  vyrgpeeegd  mlnpglvmtg  tkcgynhicf  egqcrntsff  etegcgkkcn
661 ghgvcnnqn  chclpgwapp  fcntpghggs  idsgpmppes  vgpvvagvlv  ailvlavlml
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781 peilrkpsqp  pppppdyrl  ggsppaplp  hlsraarnsp  gpgsqierte  ssrrpppsrp
841 ippapncivs  qdfsrrppq  kalpanvpvg  rrsllprpga  splrppgagp  qqsrlaala
```

// 901 pkvsprealk vkagtrglqg grcrvektkq fmlvvwtel peqkprakhs cflvpa

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Feb 24 2004 16:01:25